

IntelliGenetics

PastDB - Past Pairwise Comparison of Sequences
Release 5.4

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Results file seq8-seq18-232-723.res made by tport on Thu 27 Oct 105 16:23:23-PST.

Query sequence being compared: US-10-756-778-8 (1-492)
 Number of sequences searched: 1
 Number of scores above cutoff: 1

Results of the initial comparison of US-10-756-778-8 (1-492) with:
File : rooke778.pep

	100-	50-	0
N			
U			
M			
B			
E			
R			
O			
P			
S			
E			
Q			
U			
E			
N			
C			
E			
S			
SCORE	54	107	161
STDEV	215	268	322
	376	429	483

PARAMETERS

	PAM-150	K-tuple
Similarity matrix	164	
Threshold level of sim.	1	Joining penalty
Mismatch penalty	5.00	Window size
Gap penalty	0.05	
Gap size penalty	1	
Cutoff score	0	
Randomization group	0	

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	483	0	0.00

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues:	492
Number of sequences searched:	1
Number of scores above cutoff:	1

The scores below are sorted by initial score.

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A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.
1	Seq18-232-723 Sequence 18	492	483	484
	Application US/			
		492	483	484
				0.00
				0

1. US-10-756778-0 (1-492)

Seq10232327231Sequence 18, Application US/10756778

Initial Score	=	483	Optimized Score	=	484	Significance	=	0.00
Residue Identity	=	98	Matches	=	477	Mismatches	=	14
Gaps	=	0	Conservative Substitutions	=	1			

X	10	20	30	40	50	60	70
IAEPPTGVINQFRI	LNDFIKYIAK	IQSTNOSD	LOYPVLT	PLRAOACV	MHLMLL	KDATT	SVWGQIDSO
MAEPPTGVINQFRI	LNDFIKYIAK	IQSTNOSD	LOYPVLT	PLRAOACV	MHLMLL	KDATT	SVWGQIDSO
X	10	20	30	40	50	60	70
OLNGYKAEILRLI	KVYTNVNTY	NOGLELEK	APLNTSD	PEYLQACR	POISVLR	SNFKVEMK	WKNVAKYK
QLNGYKAEILRLI	KVYTNVNTY	NOGLELEK	APLNTSD	PEYLQACR	POISVLR	SNFKVEMK	WKNVAKYK
150	160	170	180	190	200	210	
RCMAMSA	LSLAALPPT	GPNYPKOAL	KVQSRQI	FAPVIGI	PGGIT	SQDSGPT	FGSMRFDVKTVDQIDALRR
RCMAMSA	LSLAALPPT	GPNYPKOAL	KVQSRQI	FAPVIGI	PGGIT	SQDSGPT	FGSMRFDVKTVDQIDALRR
150	160	170	180	190	200	210	
220	230	240	250	260	270	280	
LMELYI	QPLKSAYFI	YESDKWKRAT	VYNDYIGKRS	NTGAHWM	SSDP	SAITYS	SALGAAGYAPNVGVRY
LMELYI	QPLKSAYFI	YESDKWKRAT	VYNDYIGKRS	NTGAHWM	SSDP	SAITYS	SALGAAGYAPNVGVRY
220	230	240	250	260	270	280	
290	300	310	320	330	340	350	360
SHGGSY	TGMAPANT	NAYAPPE	KYCGKL	HSVAYGL	SKAPDA	ADSVWFG	FRPVLLENANQLTTALQI
SHGGSY	TGMAPANT	NAYAPPE	KYCGKL	HSVAYGL	SKAPDA	ADSVWFG	FRPVLLENANQLTTALQI
290	300	310	320	330	340	350	360
PAEIGIT	DVPAFGRTE	PIPINGOD	AIRESFT	SGFGFT	YTVDS	PQKOKY	KIIVRIANNLSASTVSLTYNNO
PAEIGIT	DVPAFGRTE	PIPINGOD	AIRESFT	SGFGFT	YTVDS	PQKOKY	KIIVRIANNLSASTVSLTYNNO
370	380	390	400	410	420	430	
440	450	460	470	480	490	X	
TFPTDIL	NTSLDP	NGVRGNT	YSVTL	VEGPIIR	FSQGTNI	IFKGSQ	KGPAIDSIIPSPVW
TFPTDIL	NTSLDP	NGVRGNT	YSVTL	VEGPIIR	FSQGTNI	IFKGSQ	KGPAIDSIIPSPVW
440	450	460	470	480	490	X	